IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of	)
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Thomas C. Hart et al.	)
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Serial No. Not yet assigned	)
	)
Filed: January 25, 2002	)
	)
For: "Methods and Compositions For Diagnosing Palmoplantar Keratodermas And Dysplasias and Other Periodontal Diseases"	)

The present application is based on International Application PCT/US00/20400. Before calculation of the filing fee, please amend the above-referenced patent application as follows:

In the specification:

At page 1, line 2, please insert the following priority claim:

-- This application is a 35 U.S.C. §371 application which claims priority to PCT/US00/20400 filed July 27, 2000 which in turn claims priority to U.S. Provisional Applications, 60/145,644 and 60/165,016 filed July 27, 1999 and November 12, 1999 respectively, the disclosure of each of these applications being incorporated herein by reference.

Please amend the specification at page 80 to include a copy of the abstract which is attached hereto on a separate sheet.

In the claims:

25. The method of claim 13 wherein a germline alteration is detected by obtaining a first CTSC gene fragment from (a) CTSC gene genomic DNA isolated from said sample, (b) CTSC RNA

isolated from said sample or (c) CTSC cDNA made from mRNA isolated from said sample and a second CTSC gene fragment from a CTSC allele specific for one of said alterations, said second fragment corresponding to said first fragment, forming single-stranded DNA from said first CTSC gene fragment and from said second CTSC gene fragment, forming a heteroduplex consisting of single-stranded DNA from said first CTSC gene fragment and single-stranded DNA from said second CTSC gene fragment and analyzing for the presence of a mismatch in said heteroduplex, wherein no mismatch indicates the presence of said alteration.

26. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of a C for a T at nucleotide position 856 in Exon 6, thereby replacing a codon encoding glutamine for a stop codon.

27. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of an A for a G at nucleotide position 857 in Exon 6, thereby replacing a codon encoding glutamine for an arginine encoding codon.

28. A method as claimed in claim 13, wherein said germline alteration comprises a deletion of an A at nucleotide position 1047 in Exon 7, thereby causing a frameshift and a premature stop codon.

29. A method as claimed in claim 13, wherein said germline alteration comprises a deletion of a dinucleotide CT at nucleotide positions 1028 and 1029 in Exon 7, thereby causing a premature stop codon.

30. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of a G for a A at nucleotide position 1286 in Exon 7, thereby replacing a

tryptophan codon with a premature stop codon.

31. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of a C for a T at nucleotide position 1015 in Exon 7, thereby replacing a codon encoding arginine for a cysteine encoding codon.

32. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of an A for a G at nucleotide position 1019 in Exon 7, thereby replacing a codon encoding tyrosine for a cysteine encoding codon.

33. A method as claimed in claim 13, wherein said germline alteration comprises a substitution of an A for a G at nucleotide position 1040 in Exon 7, thereby replacing a codon encoding tyrosine for a cysteine encoding codon.

34. A method for detecting a germline alteration in a CTSC human encoding nucleic acid, said method comprising comparing a sequence of a CTSC DNA or CTSC RNA from a human sample with an isolated wild type CTSC sequence as provided in SEQ ID NO:1.

35. A method as claimed in claim 34, wherein stability of said altered CTSC mRNA is compared with stability of wild type CTSC mRNA.

36. A method as claimed in claim 34, further comprising expressing an altered CTSC protein from said altered CTSC encoding nucleic acid and comparing cathepsin C enzymatic activity of said altered CTSC protein to enzymatic activity of wild-type cathepsin C.

37. A kit for detecting the presence of an altered CTSC encoding nucleic acid in a biological sample, comprising:

i) oligonucleotides which specifically hybridize with CTSC encoding nucleic acids having the alterations set forth in Table 1;

ii) reaction buffer; and

iii) an instruction sheet.

38. A kit as claimed in claim 37, wherein said oligonucleotide contains a tag.

39. A kit for detecting the presence an altered CTSC encoding nucleic acid in a biological sample, comprising:

i) antibodies immunologically specific for the altered CTSC proteins of the invention;

ii) a solid support with immobilized CTSC antigens as a positive control; and

iii) an instruction sheet.

40. A kit as claimed in claim 39, wherein said antibody contains a tag.

REMARKS

The purpose of this preliminary amendment is to 1) correct a minor error in the numbering of the claims; 2) insert a priority claim into the specification and 3) provide a copy of the abstract on a separate sheet.

Favorable consideration leading to prompt allowance of the present application is respectfully requested.

Respectfully submitted,
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By